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RAW SEQUENCE LISTING

DATE: 01/25/2002

PATENT APPLICATION: US/09/808,885

TIME: 17:00:10

Input Set : N:\Crf3\RULE60\09808885.raw

Output Set: N:\CRF3\01252002\I808885.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Hillman, Jennifer
6 Corley, Neil C.
7 Shah, Purvi
9 (ii) TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
11 (iii) NUMBER OF SEQUENCES: 3
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15 (B) STREET: 3174 Porter Drive
16 (C) CITY: Palo Alto
17 (D) STATE: CA
18 (E) COUNTRY: USA
19 (F) ZIP: 94304
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Diskette
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: DOS
25 (D) SOFTWARE: FastSEQ for Windows Version 2.0
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/09/808,885
C--> 29 (B) FILING DATE: 14-Mar-2001
30 (C) CLASSIFICATION:
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 09/295,055
34 (B) FILING DATE:
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Billings, Lucy J.
38 (B) REGISTRATION NUMBER: 36,749
39 (C) REFERENCE/DOCKET NUMBER: PF-0354 US
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: 415-855-0555
43 (B) TELEFAX: 415-845-4166
44 (C) TELEX:
47 (2) INFORMATION FOR SEQ ID NO: 1:
49 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 290 amino acids
51 (B) TYPE: amino acid
52 (C) STRANDEDNESS: single
53 (D) TOPOLOGY: linear
55 (vii) IMMEDIATE SOURCE:
56 (A) LIBRARY: PROSNON01
57 (B) CLONE: 2272281

ENTERED

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59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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61 Met Lys Arg Asn Ser Pro Gln Lys Ile Lys Lys Arg Lys Asp Arg Arg
62 1 5 10 15
63 Ala Lys Lys Gln Ser Phe Asp Asp Asn Asp Ser Glu Glu Leu Glu Asp
64 20 25 30
65 Lys Asp Ser Lys Ser Lys Lys Thr Ala Lys Pro Lys Val Glu Met Tyr
66 35 40 45
67 Ser Gly Ser Asp Asp Asp Asp Asp Phe Asn Lys Leu Pro Lys Lys Ala
68 50 55 60
69 Lys Gly Lys Ala Gln Lys Ser Asn Lys Lys Trp Asp Gly Ser Glu Glu
70 65 70 75 80
71 Asp Glu Asp Asn Ser Lys Lys Ile Lys Glu Arg Ser Arg Ile Asn Ser
72 85 90 95
73 Ser Gly Glu Ser Gly Asp Glu Ser Asp Glu Phe Leu Gln Ser Arg Lys
74 100 105 110
75 Gly Gln Lys Lys Asn Gln Lys Asn Lys Pro Gly Pro Asn Ile Glu Ser
76 115 120 125
77 Gly Asn Glu Asp Asp Asp Ala Ser Phe Lys Ile Lys Thr Val Ala Gln
78 130 135 140
79 Lys Lys Ala Glu Lys Lys Glu Arg Glu Arg Lys Lys Arg Asp Glu Glu
80 145 150 155 160
81 Lys Ala Lys Leu Arg Lys Leu Lys Glu Lys Glu Glu Leu Glu Thr Gly
82 165 170 175
83 Lys Lys Asp Gln Ser Lys Gln Lys Glu Ser Gln Arg Lys Phe Glu Glu
84 180 185 190
85 Glu Thr Val Lys Ser Lys Val Thr Val Asp Thr Gly Val Ile Pro Ala
86 195 200 205
87 Ser Glu Glu Lys Ala Glu Thr Pro Thr Ala Ala Glu Asp Asp Asn Glu
88 210 215 220
89 Gly Asp Lys Lys Lys Lys Asp Lys Lys Lys Lys Lys Gly Glu Lys Glu
90 225 230 235 240
91 Glu Lys Glu Lys Glu Lys Lys Lys Gly Pro Ser Lys Ala Thr Val Lys
92 245 250 255
93 Ala Met Gln Glu Ala Leu Ala Lys Leu Lys Glu Glu Glu Glu Arg Gln
94 260 265 270
95 Lys Arg Glu Glu Glu Glu Arg Ile Lys Arg Leu Glu Glu Leu Glu Ser
96 275 280 285
97 Lys Pro
98 290

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100 (2) INFORMATION FOR SEQ ID NO: 2:

102 (i) SEQUENCE CHARACTERISTICS:

103 (A) LENGTH: 1434 base pairs

104 (B) TYPE: nucleic acid

105 (C) STRANDEDNESS: single

106 (D) TOPOLOGY: linear

108 (vii) IMMEDIATE SOURCE:

109 (A) LIBRARY: PROSNON01

110 (B) CLONE: 2272281

112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/808,885

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Input Set : N:\Crif3\RULE60\09808885.raw

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114 CTGTTCCAGT GCGCGGGTCT GTGGAGAGCC GGGTGCGAGC GGCGGCAGCA CGAGGGGAAA      60
115 AGAGCTGAGC GGAGACCAAA GTCAGCCGGG AGACAGTGGG TCTGTGAGAG ACCGAATAGA      120
116 GGGGCTGGGG CCACGAGCGC CATTGACAAG CAATGGGGAA GAAACAGAAA AACAAGAGCG      180
117 AAGACAGCAC CAAGGATGAC ATTGATCTTG ATGCCTTGGC TGCAGAAATA GAAGGAGCTG      240
118 GTGCTGCCAA AGAACAGGAG CCTCAAAAGT CAAAAGGGAA AAAGAAAAAA GAGAAAAAAA      300
119 AGCAGGACTT TGATGAAGAT GATATCCTGA AAGAACTGGA AGAATTGTCT TTGGAAGCTC      360
120 AAGGCATCAA AGCTGACAGA GAAACTGTTG CAGTGAAGCC AACAGAAAAC AATGAAGAGG      420
121 AATTCACCTC AAAAGATAAA AAAAAGAAAG GACAGAAGGG CAAAAAACA GAGTTTTGAT      480
122 GATAATGATA GCGAAGAATT GGAAGATAAA GATTCAAAAT CAAAAAGAC TGCAAAACCG      540
123 AAAGTGGAAG TGTACTCTGG GAGTGATGAT GATGATGATT TTAACAACT TCCTAAAAAA      600
124 GCTAAAGGGA AAGCTCAAAA ATCAAATAAG AAGTGGGATG GGTCAGAGGA GGATGAGGAT      660
125 AACAGTAAAA AAATTAAAGA GCGTTCAAGA ATAAATTCTT CTGGTGAAAG TGGTGATGAA      720
126 TCAGATGAAT TTTTGCAATC TAGAAAAGGA CAGAAAAAAA ATCAGAAAAA CAAGCCAGGT      780
127 CCTAACATAG AAAGTGGGAA TGAAGATGAT GACGCCTCCT TCAAAATTAA GACAGTGGCC      840
128 CAAAAGAAGG CAGAAAAGAA GGAGCGCGAG AGAAAAAGC GAGATGAAGA AAAAGCGAAA      900
129 CTGCGGAAGC TGAAGAAGAA AGAAGAGTTA GAAACAGGTA AAAAGGATCA GAGTAAACAA      960
130 AAGGAATCTC AAAGGAAATT TGAAGAAGAA ACTGTAAAT CCAAAGTGAC TGTTGATACT     1020
131 GGAGTAATTC CTGCCTCTGA AGAGAAAGCA GAGACTCCCA CAGCTGCAGA AGATGACAAT     1080
132 GAAGGAGACA AAAAGAAGAA AGATAAGAAG AAAAAGAAAG GAGAAAAGGA AGAAAAGAG     1140
133 AAAGAGAAGA AAAAAGGACC TAGCAAAGCC ACTGTAAAG CTATGCAAGA AGCTCTGGCT     1200
134 AAGCTTAAAG AGGAAGAAGA AAGACAGAAG AGAGAAGAGG AAGAACGTAT AAAACGGCTT     1260
135 GAAGAATTAG AAAGCAAGCC GTAAGCACAA GGAACCGTTT GGAACCCAGA CCAAAGAGC     1320
136 AAGGGCACAG GCAAGACACC AAACCAAGGG GCGGCCCCCG AATTAATGTA CCTCTTCGCA     1380
137 CCGGGAATTC CTTTCGGGGC CGTTCCTGCA AGCGGAACCA ATTTCCCTA AAGG           1434

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1514949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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153 Gly Gln Lys Gly Lys Lys Thr Ser Phe Asp Glu Asn Asp Ser Glu Glu
154   1             5             10             15
155 Leu Glu Asp Lys Asp Ser Lys Ser Lys Lys Pro Ala Arg Pro Asn Ser
156           20           25           30
157 Glu Val Leu Leu Ser Gly Ser Glu Asp Ala Asp Asp Pro Asn Lys Leu
158       35           40           45
159 Ser Lys Lys Gly Lys Lys Ala Gln Lys Ser Thr Lys Lys Arg Asp Gly
160   50           55           60
161 Ser Glu Glu Asp Glu Asp Asn Ser Lys Arg Ser Lys Glu Arg Ser Arg
162   65           70           75           80
163 Val Asn Ser Ser Gly Glu Ser Gly Gly Glu Ser Asp Glu Phe Leu Gln
164       85           90           95
165 Ser Arg Lys Gly Gln Lys Lys Asn Gln Lys Asn Lys Ser Val Pro Thr
166   100          105          110
167 Ile Asp Ser Gly Asn Glu Asp Asp Asp Ser Ser Phe Lys Ile Lys Thr

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```

168          115          120          125
169 Val Ala Gln Lys Lys Ala Glu Lys Lys Glu Arg Glu Arg Lys Lys Arg
170          130          135          140
171 Glu Glu Glu Lys Ala Lys Leu Arg Lys Val Lys Glu Lys Glu Glu Leu
172 145          150          155          160
173 Glu Lys Gly Arg Lys Glu Gln Ser Lys Gln Arg Glu Pro Gln Lys Arg
174          165          170          175
175 Pro Asp Glu-Glu-Val Leu Val Leu Arg Gly Thr Pro Asp Ala Gly Ala
176          180 185          190
177 Ala Ser Glu Glu Lys Gly Asp Ile Ala Ala Thr Leu Glu Asp Asp Asn
178          195          200          205
179 Glu Gly Asp Lys Lys Lys Lys Asp Lys Lys Lys Lys Lys Thr Glu Lys
180          210          215          220
181 Asp Asp Lys Glu Lys Glu Lys Lys Lys Gly
182 225          230

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/808,885

DATE: 01/25/2002

TIME: 17:00:11

Input Set : N:\Crf3\RULE60\09808885.raw

Output Set: N:\CRF3\01252002\I808885.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]